

INFORMATION DISCLOSURE STATEMENT	Atty. Docket No.: 6241.N DV1	Serial No.: 09/991,211
	Applicant(s): Benson et al.	Confirmation No.: Unassigned
	Filing Date: November 21, 2001	Group: Unassigned 1652

U.S. PATENT DOCUMENTS


Examiner Initial	Copy Enclosed	Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
DJS	X	6,356,845	03/12/02	Benson et al.	/	/	

FOREIGN PATENT DOCUMENTS

Examiner Initial	Copy Enclosed	Document Number	Date	Country	Class	Subclass	Translation	
							Yes	No
DJS		EP 786519 A2	07/01/97	Europe	/	/		
		EP 899335 A2	03/03/99	Europe	/	/		
		WO 00/12678	03/09/00	PCT	/	/		
		WO 99/47639	09/23/99	PCT	/	/		
		WO 99/47662	09/23/99	PCT	/	/		
DJS		WO 01/16292 A2	03/08/01	PCT	/	/		

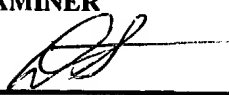
OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial	Copy Enclosed	Document Description
DJS		Arakawa et al., "Theory of Protein Solubility," <i>Methods in Enzymology</i> , 1985; 114:49-76.
		Bartlett et al., "CAVEAT: A program to facilitate the structure-derived design of biologically active molecules," <i>Molecular Recognition: Chemical and Biological Problems</i> , Royal Society of Chemistry, Special Pub No. 78:182-196 (1989).
		Benson et al., "Overexpression, Purification, and Mechanistic Study of UDP-N-Acetylenolpyruvylglucosamine Reductase," <i>Biochemistry</i> . 1993;32:2024-30.
		Benson et al., "Crystallization and preliminary X-ray crystallographic studies of UDP-N-acetylenolpyruvylglucosamine reductase," <i>Protein Science</i> . 1994; 3(7):1125-7.
DJS		Benson et al., "An enzyme-substrate complex involved in bacterial cell wall biosynthesis," <i>Nat Struct Biol</i> . 1995 (8):644-53.

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DS		Benson et al., "The structure of the substrate-free form of MurB, an essential enzyme for the synthesis of bacterial cell walls," <i>Structure</i> . 1996;4(1):47-54.
		Benson et al., "X-ray crystal structures of the S229A mutant and wild-type MurB in the presence of the substrate enolpyruvyl-UDP-N-acetylglucosamine at 1.8-A resolution," <i>Biochemistry</i> . 1997;36(4):806-11.
		Benson et al., "Kinetic characterization of wild-type and S229A mutant MurB: evidence for the role of Ser 229 as a general acid," <i>Biochemistry</i> . 1997;36(4):796-805.
	X	Benson et al., "A structural variation for MurB: X-ray crystal structure of <i>Staphylococcus aureus</i> UDP-N-Acetylenolpyruvylglucosamine reductase (MurB)," <i>Biochemistry</i> , 2001; 40(8):2340-50.
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DS		Bupp et al., "The final step of peptidoglycan subunit assembly in <i>Escherichia coli</i> occurs in the cytoplasm," <i>J. Bacteriol</i> . 1993;175:1841-3.

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DS		Chamberlain et al, "Possible arrangement of the five domains in human complement factor I as determined by a combination of X-ray and neutron scattering and homology modeling," <i>Biochemistry</i> . 1998;37:13918-29.
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		Collaborative Computational Project, No. 4, "The CCP4 suite: programs for protein crystallography" <i>Acta Cryst.</i> 1994;D50:760-3.
		Cowtan et al., "Improvement of Macromolecular Electron-Density Maps by the Simultaneous Application of Real and Reciprocal Space Constraints," <i>Acta Crystallogr D Biol Crystallogr</i> . 1993;49 (Pt 1):148-157.
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		Dobbek et al., "Crystal structure and mechanism of CO dehydrogenase, a molybdo iron-sulfur flavoprotein containing S-selanylcysteine," <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1999;96(16):8884-9.
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DS		Eisen et al., "HOOK: A program for finding novel molecular architectures that satisfy the chemical and steric requirements of a macromolecule binding site," <i>Proteins</i> . 1994;19(3):199-221.

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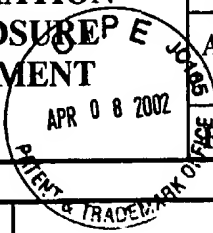
Examiner Initial	Copy Enclosed	Document Description
DJS		Evans, "SETOR: hardware-lighted three-dimensional solid model representations of macromolecules," <i>J Mol Graph.</i> 1993;11(2):134-8, 127-8.
	X	GenCore Alignment database search results for various <i>Staphylococcus aureus</i> , dated March 9, 2001.
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		Goodford, "A computational procedure for determining energetically favorable binding sites on biologically important macromolecules," <i>Med Chem.</i> 1985;28(7):849-57.
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		Hendrickson, "Determination of Macromolecular Structures from Anomalous Diffraction of Synchrotron Radiation," <i>Science.</i> 1991;254:51-8.
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DJS		Kopp et al., "Staphylococcal Peptidoglycan Interpeptide Bridge Biosynthesis: A Novel Antistaphylococcal Target?," <i>Microb. Drug. Resist.</i> 1996;2:29-41.

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DIS		Kraulis, "MOLSCRIPT: a program to produce both detailed and schematic plots of protein structures," <i>J. Appl. Cryst.</i> 1991;24:946-50.
		Kuntz et al., "A Geometric Approach to Macromolecule-Ligand Interactions," <i>J. Mol. Biol.</i> 1982;161:269-288.
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DIS		Maruyama et al., "Determination of Gene Products and Coding Regions from the <i>murE-murF</i> Region of <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> 1988;170:3786-8.

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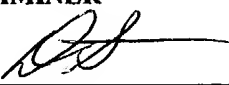
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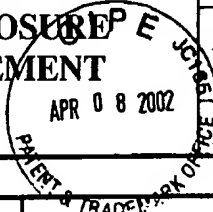
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<i>DS</i>		Mattevi et al., "Crystal structures and inhibitor binding in the octameric flavoenzyme vanillyl-alcohol oxidase: the shape of the active-site cavity controls substrate specificity," <i>Structure</i> . 1997;5:907-20.
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<i>DS</i>		Noren et al., "A General Method for Site-Specific Incorporation of Unnatural Amino Acids into Proteins," <i>Science</i> . 1989;244:182-8.

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DS		Ohringer et al., "Crystallization and preliminary crystallographic analysis of <i>E. coli</i> uridine 5'-diphospho-N-acetylenolpyruvylglucosamine reductase in two new crystal forms," <i>Acta Cryst.</i> 1996;D52:586-588.
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↓		Rossmann et al., "Chemical and biological evolution of nucleotide-binding protein," <i>Nature.</i> 1974;250(463):194-9.
DS		Sack, "CHAIN-A Crystallographic Modeling Program," <i>J. Mol. Graph.</i> 1988;6:224-25.

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DS		Sheldrick et al., "Structure Solution by Iterative Peaklist Optimization and Tangent Expansion in Space Group P1," <i>Acta Cryst.</i> 1995;B51:423-31.
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↓ DS		Zhang et al., "Crystallization and initial spectroscopic characterization of the heme-containing dehaloperoxidase from the marine polychaete <i>Amphitrite ornata</i> ," <i>Acta Crystallographica Section D Biological Crystallography.</i> 1996; 52:1191-93.

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